Morteza Sabri

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Portfolio | LinkedIn | Github | GoogleScholar | Orcid

PROFESSIONAL SUMMARY

Experienced bioinformatician specializing in bulk and single-cell RNA-Seq analysis—applied to cardiovascular and neurodevelopment research—proficient in R, Shell, and HPC. Developed pipelines accelerating analysis by 80%, identifying novel biomarkers, boosting productivity and reproducibility. Passionate about teaching and solving biological problems through bioinformatics. For more about my background and selected projects, please see my portfolio: https://mortezasabri.github.io/

HIGHLIGHTED AREAS OF EXPERTISE

- Bulk & single-cell RNA-Seq
- Data Visualization & Reproducibility
- R programming & Shell Scripting
- Study design & Data Interpretation

EXPERIENCE

Scientific Staff, Bioinformatician | RWTH Aachen University, Aachen **Jan 2025 – Apr 2025**

- Performed single-cell RNA-Seq analysis to study neuron migration in the absence of DNMT1.
- Conducted methylation array data analysis on 64 subjects with postpartum depression.
- Handled data preprocessing (Parse Bioscience's Trailmaker), statistical analysis, and visualization (R).

Scientific Staff, Bioinformatician | Technical University of Munich, Munich **Nov 2023 - Nov 2024**

- Conducted bulk and single-cell RNA-Seq analyses for cardiovascular research.
- Managed workflows from raw data to functional interpretation and identifying new biomarkers.
- Generated publication-ready visualizations illustrating gene-disease associations.
- Optimized preprocessing pipelines with R/Shell scripting, reducing runtime up to 80%.

Guest Scientist, Bioinformatician | Helmholtz Munich, Munich **Oct 2024 - Nov 2024**

- Performed deconvolution analysis to interpret bulk RNA-Seq datasets using BayesPrism R package to elucidate cell-type composition.

Instructor & Freelance, Bioinformatician | Self-Employed, Tehran **2019 – 2022**

- Delivered over 10 onsite workshops on R programming, RNA-Seq, and Linux/Shell scripting.
- Provided freelance bioinformatics services including RNA-Seq, epigenomics, and visualization.
- Supported manuscript revisions by performing advanced statistical analyses (e.g., MINT).

SKILLS

Laboratory Techniques:

- RNA/DNA extraction
- PCR & qRT-PCR
- Primer design

Programming Languages:

- R
- Shell/Bash
- Markdown & LaTeX
- Git & GitHub
- MATLAB (basic)
- Python (basic)

Bioinformatics Workflows:

- Bulk & single-cell RNA-seq
- ChIP-Seq
- Genome Assembly
- Expression & Methylation Arrays

Software and HPC:

- CLC Genomics Workbench
- Galaxy
- Jupyter Notebooks
- SPSS
- Sherlock & RWTH Aachen cluster

EDUCATION

M.Sc. Biology (Genetics), University of Sistan and Baluchestan, Iran

- **Thesis**: "Investigation of Superoxide Dismutase and Catalase Gene Expression under Drought Stress: A Comparative Study between Sistan and Baluchestan and Moderate Cultivars".

B.Sc. Cellular and Molecular Biology (Genetics), Islamic Azad University, Iran

CERTIFICATIONS & LANGUAGES

TOEFL iBT, ETS - Score: 110, February 2023
Languages: Persian (Native), English (Proficient), Azeri (Basic)

AWARDS/RECOGNITIONS/VOLUNTEER WORK

Biocast101 podcast (Apple, Spotify, Castbox, PodLink) Since 2021
Bioinformatics101 on social media (YouTube, Instagram, etc) Since 2019

PUBLICATION

Overcoming trastuzumab resistance in HER2-positive breast cancer, Journal of Cellular Physiology, 2019. DOI: 10.1002/jcp.29216

Evaluation of monolignol biosynthesis gene network in Camelina sativa, Agricultural Biotechnology Journal, 2020.

Investigation of Superoxide Dismutase and Catalase Gene Expression under Drought Stress: A Comparative Study between Sistan and Baluchestan and Moderate Cultivars – (Draft)

TEACHING EXPERIENCE

Workshops: R & Linux/Shell programming, RNA-Seq, Visualization and basic stats in R
Certificates on my portfolio

HIGHLIGHTED PIPELINES

- Bulk RNA-Seq (STAR/HISAT2 → DESeq2/edgeR → GO/KEGG)
- scRNA-Seq (Seurat & SingleCellExperiment)
- Genome assembly (Velvet, SPAdes)
- Epigenomic analyses (limma on IDAT files)

More details on my portfolio

INTERESTS

Genome editing, Machine learning, Comparative genomics, Data science, Computer science
Climbing, Hiking, Camping, Mountaineering

REFERENCE

Prof. Dr. Lars Mägdefessel lars.maegdefessel@tum.de
Dr. Mahboubeh Yazdanifar maribel.yazdanifar@myome.com
Dr. Komeil Razmi komeil.razmi@csiro.au